

Amendments to the Claims

The listing of claims will replace all prior versions, and listings of claims in the application.

1-21. (canceled)

22. (currently amended) A genetic vector for stable transfection and expression of a desired protein within eukaryotic cells comprising:

- (a) distal 5' flanking sequences of a eukaryotic locus;
- (b) proximal 5' regulatory sequences of a eukaryotic locus;
- (c) at least a first insertion site for a first heterologous coding sequence;

and

(d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and wherein

(1) said distal 5' flanking sequences comprise a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; ~~or~~

(2) said proximal 5' regulatory sequences comprise a sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus; and

(3) said proximal 3' regulatory sequences comprise a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found within the proximal 3' regulatory sequences of a ferritin heavy chain gene locus.

23. (currently amended) A genetic vector for stable transfection and expression of a desired protein within eukaryotic cells comprising:

- (a) distal 5' flanking sequences of a eukaryotic locus;
- (b) proximal 5' regulatory sequences of a eukaryotic locus;
- (c) at least a first heterologous coding sequence encoding said desired protein; and
- (d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and wherein

(1) said distal 5' flanking sequences comprise a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; or

(2) said proximal 5' regulatory sequences comprise a sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus; and

(3) said proximal 3' regulatory sequences comprise a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found within the proximal 3' regulatory sequences of a ferritin heavy chain gene locus.

24. (previously presented) A genetic vector of claim 22 wherein said distal 5' flanking sequences are derived from a ferritin heavy chain locus.

25. (previously presented) A genetic vector of claim 22 wherein said proximal 5' regulatory sequences are derived from a ferritin heavy chain locus.

26. (previously presented) A genetic vector of claim 22 wherein said proximal 5' regulatory sequences and said 5' distal flanking sequences are derived from a ferritin heavy chain locus.

27. (previously presented) A genetic vector of claim 22 wherein said proximal 3' regulatory sequences are derived from a ferritin heavy chain locus.

28. (previously presented) A genetic vector of claim 22 further comprising distal 3' flanking sequences of a ferritin heavy chain locus.

29. (previously presented) A genetic vector of claim 22 wherein said insertion site for a heterologous sequence includes at least one restriction endonuclease site.

30. (previously presented) A genetic vector as in claim 29 wherein said insertion site for a heterologous sequence is a polylinker site including at least two restriction endonuclease sites.

31. (previously presented) A genetic vector of claim 22 wherein said proximal 5' regulatory sequences include a eukaryotic intron sequence.

32. (previously presented) A genetic vector as in claim 31 wherein said eukaryotic intron sequence is derived from intron 1 of a ferritin heavy chain gene.

33. (previously presented) A genetic vector of claim 22 wherein said proximal 5' regulatory sequences include untranslated exon sequences.

34. (previously presented) A genetic vector of claim 22 wherein said distal 5' flanking sequences and said proximal 5' regulatory sequences have a total length of between 1,000 and 10,000 bases.

35. (previously presented) A genetic vector of claim 22 wherein said proximal 3' regulatory sequences and any distal 3' flanking sequences have a total length of between 1,000 and 10,000 bases.

36. (previously presented) A genetic vector of claim 22 wherein said distal 5' flanking sequences comprise a sequence having at least 80% identity to said nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus.

37. (previously presented) A genetic vector of claim 22 wherein said distal 5' flanking sequences comprise a sequence having at least 90% identity to said nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus.

38. (previously presented) A genetic vector of claim 22 wherein said distal 5' flanking sequences comprise a sequence having 100% identity to said nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus.

39. (previously presented) A genetic vector of claim 22 wherein said distal 5' flanking sequences comprise a sequence of at least 500 bases having at least 70% identity to said nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus.

40. (previously presented) A genetic vector of claim 22 wherein said distal 5' flanking sequences comprise a sequence of at least 1,000 bases having at least 70% identity to said nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus.

41. (previously presented) A genetic vector of claim 22 wherein said proximal 5' regulatory sequences comprise a sequence having at least 80% identity to said nucleotide

sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

42. (previously presented) A genetic vector of claim 22 wherein said proximal 5' regulatory sequences comprise a sequence having at least 90% identity to said nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

43. (previously presented) A genetic vector of claim 22 wherein said proximal 5' regulatory sequences comprise a sequence having 100% identity to said nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

44. (previously presented) A genetic vector of claim 22 wherein said proximal 5' regulatory sequences comprise a sequence of at least 500 bases having at least 70% identity to said nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

45. (previously presented) A genetic vector of claim 22 wherein said proximal 5' regulatory sequences comprise a sequence of at least 1,000 bases having at least 70% identity to said nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

46. (previously presented) A genetic vector of claim 22 wherein the length of said first insertion site is 0, 1, 2 or 3 bp.

47. (previously presented) A genetic vector of claim 22 wherein the length of said first insertion site is 4 bp.

48. (previously presented) A genetic vector of claim 22 wherein the length of said first insertion site is 1,000 bp.

49. (previously presented) A genetic vector of claim 22 wherein the length of said first insertion site is 5,000 bp.

50. (canceled)

51. (previously presented) A genetic vector of claim 22 wherein said proximal 3' regulatory sequences comprise a sequence having at least 80% identity to a nucleotide sequence found within the proximal 3' regulatory sequences of a ferritin heavy chain locus.

52. (previously presented) A genetic vector of claim 22 wherein said proximal 3' regulatory sequences comprise a sequence having at least 90% identity to a nucleotide sequence found within the proximal 3' regulatory sequences of a ferritin heavy chain locus.

53. (previously presented) A genetic vector of claim 22 wherein said proximal 3' regulatory sequences comprise a sequence having 100% identity to a nucleotide sequence found within the proximal 3' regulatory sequences of a ferritin heavy chain locus.

54. (canceled)

55. (previously presented) A genetic vector of claim 22 wherein said proximal 3' regulatory sequences comprise at least 1,000 nucleotides.

56. (previously presented) A genetic vector of claim 22 wherein said proximal 3' regulatory sequences consist essentially of a polyadenylation signal.

57. (previously presented) A genetic vector of claim 22 further comprising a distal 3' flanking sequence of a eukaryotic locus comprising a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

58. (previously presented) A genetic vector of claim 57 wherein said distal 3' flanking sequence comprises a sequence having at least 80% identity to said nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

59. (previously presented) A genetic vector as in claim 57 wherein said distal 3' flanking sequence comprises a sequence having at least 90% identity to said nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

60. (previously presented) A genetic vector as in claim 57 wherein said distal 3' flanking sequence comprises a sequence having 100% identity to said nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

61. (previously presented) A genetic vector as in claim 57 wherein said distal 3' flanking sequence comprises a sequence of at least 500 bases having at least 70% identity to said nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

62. (previously presented) A genetic vector as in claim 57 wherein said distal 3' flanking sequence comprises a sequence of at least 1,000 bases having at least 70% identity to said nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

63. (previously presented) The genetic vector pFerX8.

64. (previously presented) The genetic vector pFerX11.

65. (previously presented) A eukaryotic cell transfected with a vector of claim 22.

66. (previously presented) A eukaryotic cell of claim 65 wherein said vector has stably integrated into a chromosome of a said cell.

67. (previously presented) A eukaryotic cell of claim 65 wherein said first coding sequence is expressed in said cell.

68. (currently amended) A eukaryotic cell comprising:

- (a) distal 5' flanking sequences of a eukaryotic locus;
- (b) proximal 5' regulatory sequences of a eukaryotic locus;
- (c) at least a first coding sequence; and
- (d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and wherein

(1) said distal 5' flanking sequences comprise an exogenous sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus;
or

(2) said proximal 5' regulatory sequences comprise an exogenous sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found

between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus; and

(3) said proximal 3' regulatory sequences comprise a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found within the proximal 3' regulatory sequences of a ferritin heavy chain gene locus.

69. (canceled)

70. (previously presented) A method of producing a desired protein in a eukaryotic cell comprising:

- (a) providing at least one cell of claim 65 or a descendent thereof;
- (b) maintaining said cell in a culture under conditions which permit high expression of said desired protein; and
- (c) isolating said desired protein from said culture.